



**FIG. 1**

1 GTCGACTTAT TGCATTGATG GCGTACATGG TAGTGCCATC CTTCTTTTGC TAACAAGCGT TGTATAAAAG  
71 CTGTGGTCGGT TTCAATCAAGT TGAACACAAT ACTCATGATT TTTCCCACTT CCGGAAAGGG AAAAGTGAAG  
141 ATAGCTTTTG AGATCAGCCT GTTCTAGCAG CTTTCAATG ATCTTTTTCG TCGTTACGTT TTGAAAAATC  
211 TGACGACTGC GTTGTATTG CAACAAGCTA AGTGGATCCA ATATCTCTAT TTGATAATAA AACTGCTGCT  
281 TGTCTTTGCT ATATCTGTG AATTGCAGAG TGCTACATAT ACCTGAAAAA AAACGCTTTC CAGAATCTAA  
351 TTCGTAAGAC ACACAAACAG CTTTACCTAG GTTTTGGTA TCGATCTCCA TGTTGCCGC GATGGAAACG  
421 GAAACTGAC ACCCGCCGGA TACGCTTCC TCTCCGATTA ATTGGGTGAC AATATAACTT TTGCTATCTG  
491 AAAGCTTAAT GGTGAGGGAG CGGGTTGGT GCTTTAATTC GTTACTGCTC ATATTCAATT AATTCACTAT  
561 TAAATAAACA GTTCTAAAG GCTGTTTATT GGATGAATAT TCGAAATTAT CACATAATAA TTGATGCTAT  
631 TATTACTTGC TGTATTGGA TCAACTTCA TGCTCTATAC ATGTAATATA TTTCGAGTTA GACCTTAATT  
701 CAAGGTAATT TGTCTATTA ATTATTATCT GAATAATATG TAATCGATTG CTTTGTGGTT ATTTTATGT  
771 TTGTTTCATT TTTAATGACG GTGAGCTTGT GCATTCATAT TTTTATGAT GACAACATCT TTGATGAAGT  
841 ATTTAAGATA TTGTTAATGC ATGAGGGGTT TCGGTGTATT TTTTATATTA AATCATAATA AAATCAACAA  
911 TATATGTTAT TTGTGTCTT TTTATAGTG TCTTTAAAG AGGTAGGATG ACCTAAAGGT CGCTTAAATA  
981 TGGCGTAAAT TGCCATTGCT ATAATTCACC TCAAAGATAC ACTATTGGCA AATIGACAAA TATGTCATT  
1051 CGTATGAAAC AAATATTAGTA GATGTTGTT TTGCTGCAAA AATAAAAAATT TTTCTGGTTG AAATAACTCA  
1121 AGGCCTCTAG CGTTTTCTT TATCTTAAAA TACAGGAAAT AGCGATTGAA GTTAATTGAC ACTTAAGCAA  
1191 ATAGTCAACC TAACAGAGCA <sup>S-D</sup> CGAACCTATG <sup>ORF A/mmp4</sup> CTTTGTCAA AGCATCAAAT TGAGCAACTT TCTAAACCTC  
1261 TGAGTGATGA TTGATCTGT GGCCTTATC TAAACTGGA AAAAAGTGCT TTTCGCCAT TACGTAATGA  
1331 ATTTAATGTC GCGCAAACTG CGCTGCGTAA GCTAAGTCAA AACCTAGTG CTGACGAGAG AGATGCGTTA  
1401 CAAGAGGCA TGTCTAAATA AGTGAAGAT TCTCTGAC AGTTGTACG AACAGTTTC AAAACAACC  
1471 AGAGATATCG AGCTCATCTC ATGGTTTGT GCTGCTCAAT TCTTCTCGA TACCACATTA GAAAGTGCTG  
1541 CGAATAGCCT TGAGTGGTTA GCGGATTAA GTGAGAAGCA CTGGGATCAC CTCAACCTG TACTACCAGT  
1611 TGAACGCTC AAATCTGATG ATGATAAGGG CAAAGAAAAG GAGCAAGCAG ATGCGAAAGT TAAAGCATT  
1681 TTCCAAC TAG CGCGCATAG CGAGGAAAGC TCGATTCTCT ATCGCCCGT GCTGCAACTG CCCTTAGTCG  
1751 GGGAAAGTAC GTTTTTGAC TTTCAAAGT CAGAGAGAAA AGGCGAAATC AGCCAACGTA AATCTATGCT  
1821 TACGACCACG GTGGCGCAAG AGCGTTTCCG AATTCAATC AAGATGGAAA ACGCCAACG TTGTGTCACC  
1891 CAATTAGATC GTTTGTCAGC GTTGGTGAGC ACTAAGTGTC ATTCTTAGG CAGTCAAAGT ACCAAGCTCG  
1961 GATTTGCGAA GTCAGTCTT ACCCGTGTG AAAACGCTT GGTTCATCTA AGTGAATTA AGTTAGCACC  
2031 GAAAGCGGAG GCCAAGACAG TAGAGCAAGA GGTGCGGAA AGTTCAAGTT CTGAAGGGGA  
GCTGCCAAGC  
2101 CATATGGATA CAAAACATAT AGAGCGAATA CCGATGGCAT CAGAGCAGGC TCAGACCGTA AGCCAACACT  
2171 TACACGCAGG AAACCTCTCT GAATCGGTA ATTTAAACAA TATGAACCGA GACTTAGCTT TCCATTGTT  
2241 GAGAGAAGTC TCTGATTATT TTGCCAGAG CGAACCGCAT AGCCCAATTT CATTTTTGT AGAAAAAGCG  
2311 ATTCGATGGG GATATTATC CTTACCTGAG TTGCTCGAG AAATGATGTC GGAACAAAAC GGTGACGCTC  
2381 TTAGTACGAT TTTAATGCC GCCGGATTGA ATCATCTCGA TCAGGTTTTG CTGCCGAGG TGAGTACTCC  
2451 AACGGTGGG ATTGAAAGCC CCCAAACACC TCAAGCGAAG CCTTCCGTTT CGGATCCCGG AAGTGTGAA  
2521 GAGCATGTAT CTCAGACTTC CCCTGTAGAT ACCCAATCTA AGCAAGATCA AAAACCAACAA TCATCCGCTA  
2591 CGTCGGCTCT GAGTTGGTAA <sup>\*</sup> TTGTGTTAA AAAATAAGGA <sup>S-D</sup> AAAATCATGG <sup>ORF B</sup> CAAGTATTA CATGCGTGTA  
2661 AGCGGTCTTC AAGTTGAGGG CGCAGCGACT ATCGGTCAGC TAGAAACGGC TGAAGGTAAA AATGACGGTT  
2731 GGTTGCAAT CAATCTTAC TCTTGGGGT GCGCTCGTAA CGTTGCTATG GACATCGGTA ACGGCACCAA  
2801 TGCGGATTCA GGCATGGTT GCGTAAGCGA AGTTAGCGTA ACTAAAGAAG TCGATGGTGC TTCTGAAGAC  
2871 CTACTGTCTT ATTTATTCAA CCCAGGTAAA GACGGTAAAA CTGTTGAGGT TGCATTACT AAGCCTCTA  
2941 ACGATGGTCA AGGTGCAGAC GTTACTTCC AAGTTAAGCT AGAAAAAGCA CGTTAGTTT CTTACAACGT  
3011 GAGCGGGACT GACGGATCTC AACCGTACGA GAGCCTATCT CTTCTTACA CTCTATTTC TCAGAAGCAT  
3081 CACTATGAGA AAGAAGGTGG TGAACACAA AGCGGTGGT TTGTGACTTA CGACCTACCG ACCGGGAAAA  
3151 TGACTTCTGG TAAGTAAATC <sup>S-D</sup> TTTCAATTAGA <sup>ORF C</sup> CATGCCACGT TAATTGGCAT GTCTATTICA TGAATATCTC  
3221 ATTTTAGGAC ACCGTTATGG CATTGAACTC ACAACATAAG CCGTTAGTA AGAACCGGT CAGCATCAC  
3291 CTATGACGTT GAAACGAATG GCGCCGTAAA GACGAAAGAG CTGCCGTTTG TTGTTGGCGT CATTGGCGAC  
3361 TTTTCAGGAC ACAACCCAGA ATCAGAAAAA GTTGATTAG AAGAGCGAGA GTTCACGGGT ATCGATAAAG  
3431 ACAACTTGA TACAGTGATG GGGCAAAATC ACCCGCTCT TTCGTACAAG GTTGATAACA AGCTTGCTAA  
3501 TGATGATAGC CAGTTGAAG TGAAGTTGAG CCTCGGTTG ATGAAAGATT TCCACCCAGA GAACTTAGTT  
3571 GATNAAATTG AGCCGCTTAA

FIG. 2

1 MPLSKHQIEQLSKPLSDDSIKGVYLLKLEKSAFRPLRNEFNVAQTALRKLSQNPSADERDALQEACLNKWK  
 71 ILSDSLYEQFSKTTTRDIELISWFVAAQFLDDTTLESAANSLEWLADLSEKHWDHLNPVLPVETLKSDDDK  
 141 GKEREQADAKVKAFFQLVGDSEESSILYAPVLQLPLVGEVTFDFQSAERKGEISQLKSMLTTTVAQER  
 211 FAIQFKMENAKRCVTQLDRLSALVSTKCHSLGSQSTNFGFAKSLLTRVENALVHLSGKLPKAEAKTVE  
 281 QEVAESSVSEGELPSHMDTKHIERIPMASEQAQTVSQHLHAGNLSELGNLNNMNRDLAFHLLREVSDYFR  
 351 QSEPHSPISFLLEKAIRWGYLSLPELLREMMSEQNGDALSTIFNAAGLNHLDQVLLPEVSTPTVGIESPQ  
 421 TPQAKPSVSDPRSVEEHVSQTSPVDTQSKQDQKPQSSATSALSW\*

*FIG. 3a*

1 MASIYMRVSGLQVEGAATIGQLETAEGKNDGWFAINSYSWGGARNVAMDIGNGTNADSGMVGVSSEVSVTK  
 71 EVDGASEDLLSYLFPNGKDGKTVEVAFTKPSNDGQADVYFQVKLEKARLVSYNVSGTDGSQPYESLSLS  
 141 YTSISQKHYY EKEGGELQSGGVVVTYDLPTGKMTSGK\*

*FIG. 3b*

1 MALNSQHKRVSKNRVSITYDVETNGAVKTKELPFVVGIGDFSGHKPESEKVDLEEREFTGIDKDNFDTV  
 71 MGQIHPRLSYKVDNKLANDDSQFEVNLSLRSMKDFHPENLVDXIEPL

*FIG. 3c*